

OIEP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/932,474

DATE: 09/06/2001

TIME: 16:05:03

Input Set : A:\ES.txt

Output Set: N:\CRF3\09062001\I932474.raw

ENTERED

3 <110> APPLICANT: BENSON, Timothy
 4 PRINCE, Donald Bryan
 6 <120> TITLE OF INVENTION: CRYSTALLIZATION AND STRUCTURE DETERMINATION OF FEMA AND
 FEMA-LIKE

7 PROTEINS
 9 <130> FILE REFERENCE: 00236.US1
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/932,474

12 <141> CURRENT FILING DATE: 2001-08-17
 14 <150> PRIOR APPLICATION NUMBER: US 60/226,239
 15 <151> PRIOR FILING DATE: 2000-08-17
 17 <150> PRIOR APPLICATION NUMBER: US 60/226,269
 18 <151> PRIOR FILING DATE: 2000-08-17
 20 <160> NUMBER OF SEQ ID NOS: 3
 22 <170> SOFTWARE: PatentIn version 3.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 414
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Staphylococcus aureus
 29 <400> SEQUENCE: 1
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 34 Lys His Phe Lys His Tyr Thr Gln Ser Ile Glu Leu Tyr Asn Tyr Arg
 35 20 25 30
 37 Asn Lys Ile Asn His Glu Ala His Ile Val Gly Val Lys Asn Asp Lys
 38 35 40 45
 40 Asn Glu Val Ile Ala Ala Cys Leu Leu Thr Glu Ala Arg Ile Phe Lys
 41 50 55 60
 43 Phe Tyr Lys Tyr Phe Tyr Ser His Arg Gly Pro Leu Leu Asp Tyr Phe
 44 65 70 75 80
 46 Asp Ala Lys Leu Val Cys Tyr Phe Phe Lys Glu Leu Ser Lys Phe Ile
 47 85 90 95
 49 Tyr Lys Asn Arg Gly Val Phe Ile Leu Val Asp Pro Tyr Leu Ile Glu
 50 100 105 110
 52 Asn Leu Arg Asp Ala Asn Gly Arg Ile Ile Lys Asn Tyr Asn Asn Ser
 53 115 120 125
 55 Val Ile Val Lys Met Leu Gly Lys Ile Gly Tyr Leu His Gln Gly Tyr
 56 130 135 140
 58 Thr Thr Gly Tyr Ser Asn Lys Ser Gln Ile Arg Trp Ile Ser Val Leu
 59 145 150 155 160
 61 Asp Leu Lys Asp Lys Asp Glu Asn Gln Leu Leu Lys Glu Met Glu Tyr
 62 165 170 175
 64 Gln Thr Arg Arg Asn Ile Lys Lys Thr Ile Glu Ile Gly Val Lys Val
 65 180 185 190
 67 Glu Asp Leu Ser Ile Glu Glu Thr Asn Arg Phe Tyr Lys Leu Phe Gln
 68 195 200 205
 70 Met Ala Glu Glu Lys His Gly Phe His Phe Met Asn Glu Asp Tyr Phe
 71 210 215 220
 73 Lys Arg Met Gln Glu Ile Tyr Lys Asp Lys Ala Met Leu Lys Ile Ala

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74 225                230                235                240
76 Cys Ile Asn Leu Asn Glu Tyr Gln Asp Lys Leu Lys Ile Gln Leu Leu
77                245                250                255
79 Lys Ile Glu Asn Glu Met Met Thr Val Asn Arg Ala Leu Asn Glu Asn
80                260                265                270
82 Pro Asn Ser Lys Arg Asn Lys Ser Lys Leu Asn Gln Leu Asn Met Gln
83                275                280                285
85 Leu Ser Ser Ile Asn Asn Arg Ile Ser Lys Thr Glu Glu Leu Ile Leu
86                290                295                300
88 Glu Asp Gly Pro Val Leu Asp Leu Ala Ala Ala Leu Phe Ile Cys Thr
89 305                310                315                320
91 Asp Asp Glu Val Tyr Tyr Leu Ser Ser Gly Ser Asn Pro Lys Tyr Asn
92                325                330                335
94 Gln Tyr Met Gly Ala Tyr His Leu Gln Trp His Met Ile Lys Tyr Ala
95                340                345                350
97 Lys Ser His Asn Ile Asn Arg Tyr Asn Phe Tyr Gly Ile Thr Gly Val
98                355                360                365
100 Phe Ser Asn Glu Ala Asp Asp Phe Gly Val Gln Gln Phe Lys Lys Gly
101                370                375                380
103 Phe Asn Ala His Val Glu Glu Leu Ile Gly Asp Phe Ile Lys Pro Val
104 385                390                395                400
106 Arg Pro Ile Leu Tyr Lys Phe Ala Lys Leu Ile Tyr Lys Val
107                405                410
109 <210> SEQ ID NO: 2
110 <211> LENGTH: 419
111 <212> TYPE: PRT
112 <213> ORGANISM: Staphylococcus aureus
114 <400> SEQUENCE: 2
116 Met Lys Phe Thr Glu Leu Thr Val Thr Glu Phe Asp Asn Phe Val Gln
117 1                5                10                15
119 Asn Pro Ser Leu Glu Ser His Tyr Phe Gln Val Lys Glu Asn Ile Val
120                20                25                30
122 Thr Arg Glu Asn Asp Gly Phe Glu Val Val Leu Leu Gly Ile Lys Asp
123                35                40                45
125 Asp Asn Asn Lys Val Ile Ala Ala Ser Leu Phe Ser Lys Ile Pro Thr
126                50                55                60
128 Met Gly Ser Tyr Val Tyr Tyr Ser Asn Arg Gly Pro Val Met Asp Phe
129 65                70                75                80
131 Ser Asp Leu Gly Leu Val Asp Tyr Tyr Leu Lys Glu Leu Asp Lys Tyr
132                85                90                95
134 Leu Gln Gln His Gln Cys Leu Tyr Val Lys Leu Asp Pro Tyr Trp Leu
135                100                105                110
137 Tyr His Leu Tyr Asp Lys Asp Ile Val Pro Phe Glu Gly Arg Glu Lys
138                115                120                125
140 Asn Asp Ala Leu Val Asn Leu Phe Lys Ser His Gly Tyr Glu His His
141                130                135                140
143 Gly Phe Thr Thr Glu Tyr Asp Thr Ser Ser Gln Val Arg Trp Met Gly
144 145                150                155                160
146 Val Leu Asn Leu Glu Gly Lys Thr Pro Glu Thr Leu Lys Lys Thr Phe

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147          165          170          175
149 Asp Ser Gln Arg Lys Arg Asn Ile Asn Lys Ala Ile Asn Tyr Gly Val
150          180          185          190
152 Lys Val Arg Phe Leu Glu Arg Asp Glu Phe Asn Leu Phe Leu Asp Leu
153          195          200          205
155 Tyr Arg Glu Thr Glu Glu Arg Ala Gly Phe Val Ser Lys Thr Asp Asp
156          210          215          220
158 Tyr Phe Tyr Asn Phe Ile Asp Thr Tyr Gly Asp Lys Val Leu Val Pro
159 225          230          235          240
161 Leu Ala Tyr Ile Asp Leu Asp Glu Tyr Val Leu Lys Leu Gln Gln Glu
162          245          250          255
164 Leu Asn Asp Lys Glu Asn Arg Arg Asp Gln Met Met Ala Lys Glu Asn
165          260          265          270
167 Lys Ser Asp Lys Gln Met Lys Lys Ile Ala Glu Leu Asp Lys Gln Ile
168          275          280          285
170 Asp His Asp Gln His Glu Leu Leu Asn Ala Ser Glu Leu Ser Lys Thr
171          290          295          300
173 Asp Gly Pro Ile Leu Asn Leu Ala Ser Gly Val Tyr Phe Ala Asn Ala
174 305          310          315          320
176 Tyr Glu Val Asn Tyr Phe Ser Gly Gly Ser Ser Glu Lys Tyr Asn Gln
177          325          330          335
179 Phe Met Gly Pro Tyr Met Met His Trp Phe Met Ile Asn Tyr Cys Phe
180          340          345          350
182 Asp Asn Gly Tyr Asp Arg Tyr Asn Phe Tyr Gly Leu Ser Gly Asp Phe
183          355          360          365
185 Thr Glu Asn Ser Glu Asp Tyr Gly Val Tyr Arg Phe Lys Arg Gly Phe
186          370          375          380
188 Asn Val Gln Ile Glu Glu Leu Ile Gly Asp Phe Tyr Lys Pro Ile His
189 385          390          395          400
191 Lys Val Lys Tyr Trp Leu Phe Thr Thr Leu Asp Lys Leu Arg Lys Lys
192          405          410          415
194 Leu Lys Lys
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 421
199 <212> TYPE: PRT
200 <213> ORGANISM: Staphylococcus aureus
202 <400> SEQUENCE: 3
204 Met Glu Lys Met His Ile Thr Asn Gln Glu His Asp Ala Phe Val Lys
205 1          5          10          15
207 Ser His Pro Asn Gly Asp Leu Leu Gln Leu Thr Lys Trp Ala Glu Thr
208          20          25          30
210 Lys Lys Leu Thr Gly Trp Tyr Ala Arg Arg Ile Ala Val Gly Arg Asp
211          35          40          45
213 Gly Glu Val Gln Gly Val Ala Gln Leu Leu Phe Lys Lys Val Pro Lys
214          50          55          60
216 Leu Pro Tyr Thr Leu Cys Tyr Ile Ser Arg Gly Phe Val Val Asp Tyr
217 65          70          75          80
219 Ser Asn Lys Glu Ala Leu Asn Ala Leu Leu Asp Ser Ala Lys Glu Ile
220          85          90          95

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222 Ala Lys Ala Glu Lys Ala Tyr Ala Ile Lys Ile Asp Pro Asp Val Glu
223           100           105           110
225 Val Asp Lys Gly Thr Asp Ala Leu Gln Asn Leu Lys Ala Leu Gly Phe
226           115           120           125
228 Lys His Lys Gly Phe Lys Glu Gly Leu Ser Lys Asp Tyr Ile Gln Pro
229           130           135           140
231 Arg Met Thr Met Ile Thr Pro Ile Asp Lys Asn Asp Asp Glu Leu Leu
232 145           150           155           160
234 Asn Ser Phe Glu Arg Arg Asn Arg Ser Lys Val Arg Leu Ala Leu Lys
235           165           170           175
237 Arg Gly Thr Thr Val Glu Arg Ser Asp Arg Glu Gly Leu Lys Thr Phe
238           180           185           190
240 Ala Glu Leu Met Lys Ile Thr Gly Glu Arg Asp Gly Phe Leu Thr Arg
241           195           200           205
243 Asp Ile Ser Tyr Phe Glu Asn Ile Tyr Asp Ala Leu His Glu Asp Gly
244           210           215           220
246 Asp Ala Glu Leu Phe Leu Val Lys Leu Asp Pro Lys Glu Asn Ile Ala
247 225           230           235           240
249 Lys Val Asn Gln Glu Leu Asn Glu Leu His Ala Glu Ile Ala Lys Trp
250           245           250           255
252 Gln Gln Lys Met Glu Thr Ser Glu Lys Gln Ala Lys Lys Ala Gln Asn
253           260           265           270
255 Met Ile Asn Asp Ala Gln Asn Lys Ile Ala Lys Asn Glu Asp Leu Lys
256           275           280           285
258 Arg Asp Leu Glu Ala Leu Glu Lys Glu His Pro Glu Gly Ile Tyr Leu
259           290           295           300
261 Ser Gly Ala Leu Leu Met Phe Ala Gly Ser Lys Ser Tyr Tyr Leu Tyr
262 305           310           315           320
264 Gly Ala Ser Ser Asn Glu Phe Arg Asp Phe Leu Pro Asn His His Met
265           325           330           335
267 Gln Tyr Thr Met Met Lys Tyr Ala Arg Glu His Gly Ala Thr Thr Tyr
268           340           345           350
270 Asp Phe Gly Gly Thr Asp Asn Asp Pro Asp Lys Asp Ser Glu His Tyr
271           355           360           365
273 Gly Leu Trp Ala Phe Lys Lys Val Trp Gly Thr Tyr Leu Ser Glu Lys
274           370           375           380
276 Ile Gly Glu Phe Asp Tyr Ile Leu Asn Gln Pro Leu Tyr Gln Leu Ile
277 385           390           395           400
279 Glu Gln Val Lys Pro Arg Leu Thr Lys Ala Lys Ile Lys Ile Ser Arg
280           405           410           415
282 Lys Leu Lys Arg Lys
283           420

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/932,474

DATE: 09/06/2001

TIME: 16:05:04

Input Set : A:\ES.txt

Output Set: N:\CRF3\09062001\I932474.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

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Directory of D:\

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table_1.txt 270 KB 8/10/01

1 file(s)
Total filesize 270 KB
2 folder(s)
0 kilobytes free